



# Blast 2 Sequences results

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## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.16 [Mar-25-2007]

Matrix BLOSUM62 gap open: 11 gap extension: 1

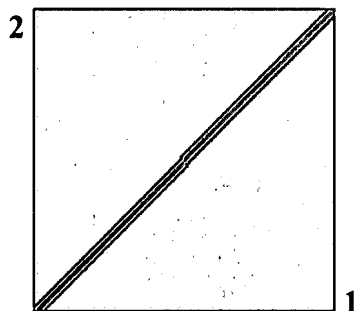
x\_dropoff: 0 expect: 10.000 wordsize: 3 Filter ☒ View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

☐ Show CDS translation 

Sequence 1: lc|seq\_1  
Length = 250 (1 .. 250)

Sequence 2: lc|seq\_2  
Length = 250 (1 .. 250)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 489 bits (1259), Expect = 8e-137, Method: Composition-based stats.  
Identities = 246/250 (98%), Positives = 248/250 (99%), Gaps = 0/250 (0%)

|       |     |                                                               |     |
|-------|-----|---------------------------------------------------------------|-----|
| Query | 1   | MAEAASCARKGTKYAEGTQPFTVLIIEGNIGSGKTTYLNHFKEYKNDICLLTEPVEKWRNV | 60  |
|       |     | MAEAASCARKGTKYAEGTQPFTVLIIEGNIGSGKTTYLNHFKEYKNDICLLTEPVEKWRNV |     |
| Sbjct | 1   | MAEAASCARKGTKYAEGTQPFTVLIIEGNIGSGKTTYLNHFKEYKNDICLLTEPVEKWRNV | 60  |
| Query | 61  | NGVNLELMEYKDPKKWAMPFQSYVTLTMLSHTAPTNNKKLIXERSIFSARYCFVENMRR   | 120 |
|       |     | NGVNLELMEYKDPKKWAMPFQSYVTLTMLSHTAPTNNKKLIERERSIFSARYCFVENMRR  |     |
| Sbjct | 61  | NGVNLELMEYKDPKKWAMPFQSYVTLTMLSHTAPTNNKKLIMERSIFSARYCFVENMRR   | 120 |
| Query | 121 | NGSLEQGMNTLEEWYKFIEESIHLQADLIILRTSPEVAYERIRQARSEESCVPLKYL     | 180 |
|       |     | NGSLEQGMNTLEEWYKFIEESIHLQADLIILRTSPEVAYERIRQARSEESCVPLKYL     |     |
| Sbjct | 121 | NGSLEQGMNTLEEWYKFIEESIHLQADLIILRTSPEVAYERIRQARSEESCVPLKYL     | 180 |
| Query | 181 | QELHELHEDWLIHQRRPQSCVKLVLDADLNLENIGTEYQRSESSIFDAISSNQPSPV     | 240 |
|       |     | QELHELHEDWLIHQRRPQSCVKLVLDADLNLENIGTEYQRSESSIFDAISSNQPSPV     |     |
| Sbjct | 181 | QELHELHEDWLIHQRRPQSCVKLVLDADLNLENIGTEYQRSESSIFDAISSNQPSPV     | 240 |
| Query | 241 | SPSKRQRVAR                                                    | 250 |
|       |     | SPSKRQRVAR                                                    |     |

Sbjct 241 SPSKRQRRVAR 250

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.



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to end

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☐ 1: Q9XZT6. Reports Deoxynucleoside k...[gi:20454871]BLink, Conserved  
Domains, Links[Comment](#) [Features](#) [Sequence](#)

LOCUS Q9XZT6 250 aa linear INV 03-APR-2007

DEFINITION Deoxynucleoside kinase (Deoxyribonucleoside kinase) (Dm-dNK)  
(Multispecific deoxynucleoside kinase).

ACCESSION Q9XZT6

VERSION Q9XZT6 GI:20454871

DBSOURCE swissprot: locus DNK\_DROME, accession Q9XZT6;  
class: standard.  
created: May 2, 2002.  
sequence updated: Nov 1, 1999.  
annotation updated: Apr 3, 2007.  
xrefs: AF045610.2, AAD47355.2, AF185268.1, AAD56545.1, Y18048.1,  
CAB41881.1, AE014297.2, AAF55615.1, 1J90A, 1J90B, 1OE0A, 1OE0B,  
1OE0C, 1OE0D, 1OT3A, 1OT3B, 1OT3C, 1OT3D, 1OT3E, 1OT3F, 1OT3G,  
1OT3H, 1ZM7A, 1ZM7B, 1ZM7C, 1ZM7D, 1ZMXA, 1ZMXB, 1ZMXC, 1ZMXD,  
1ZMXE, 1ZMXF, 1ZMXG, 1ZMXH  
xrefs (non-sequence databases): UniGene:Dm.1248, DIP:DIP:23491N,  
IntAct:Q9XZT6, Ensembl:CG5452, KEGG:dme:Dmel\_CG5452,  
FlyBase:FBgn0022338, BioCyc:DMEL-XXX-02:DMEL-XXX-02-012305-MONOMER,  
GermOnline:CG5452, GO:0019136, GO:0005515, GO:0006165,  
InterPro:IPR002624, PANTHER:PTHR10513, Pfam:PF01712

KEYWORDS 3D-structure; ATP-binding; Complete proteome; DNA synthesis;  
Kinase; Nucleotide-binding; Transferase.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM [Drosophila melanogaster](#)  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (residues 1 to 250)

AUTHORS Johansson,M., van Rompay,A.R., Degreve,B., Balzarini,J. and  
Karlsson,A.

TITLE Cloning and characterization of the multisubstrate  
deoxyribonucleoside kinase of Drosophila melanogaster

JOURNAL J. Biol. Chem. 274 (34), 23814-23819 (1999)

PUBMED [10446143](#)

REMARK NUCLEOTIDE SEQUENCE [MRNA], AND CHARACTERIZATION.

REFERENCE 2 (residues 1 to 250)

AUTHORS Munch-Petersen,B., Knecht,W., Lenz,C., Sondergaard,L. and Piskur,J.

TITLE Functional expression of a multisubstrate deoxyribonucleoside  
kinase from Drosophila melanogaster and its C-terminal deletion  
mutants

JOURNAL J. Biol. Chem. 275 (9), 6673-6679 (2000)

PUBMED [10692477](#)

REMARK NUCLEOTIDE SEQUENCE [GENOMIC DNA / MRNA], AND CHARACTERIZATION.  
STRAIN=Oregon-R

REFERENCE 3 (residues 1 to 250)

**AUTHORS** Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Baxendale, J., Bayraktaroglu, L., Beasley, E.M., Beeson, K.Y., Benos, P.V., Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottier, P., Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I., Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z., Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Liu, X., Mattei, B., McIntosh, T.C., McLeod, M.P., McPherson, D., Merkulov, G., Milshina, N.V., Mobarry, C., Morris, J., Moshrefi, A., Mount, S.M., Moy, M., Murphy, B., Murphy, L., Muzny, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Nusskern, D.R., Pacleb, J.M., Palazzolo, M., Pittman, G.S., Pan, S., Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Simpson, M., Skupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E., Svirska, R., Tector, C., Turner, R., Venter, E., Wang, A.H., Wang, X., Wang, Z.Y., Wassarman, D.A., Weinstock, G.M., Weissbach, J., Williams, S.M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, Q.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zhao, Q., Zheng, L., Zheng, X.H., Zhong, F.N., Zhong, W., Zhou, X., Zhu, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C.

**TITLE** The genome sequence of *Drosophila melanogaster*

**JOURNAL** Science 287 (5461), 2185-2195 (2000)

**PUBMED** [10731132](#)

**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
STRAIN=Berkeley

**REFERENCE** 4 (residues 1 to 250)

**AUTHORS** Misra, S., Crosby, M.A., Mungall, C.J., Matthews, B.B., Campbell, K.S., Hradecky, P., Huang, Y., Kaminker, J.S., Millburn, G.H., Prochnik, S.E., Smith, C.D., Tupy, J.L., Whitfield, E.J., Bayraktaroglu, L., Berman, B.P., Bettencourt, B.R., Celniker, S.E., de Grey, A.D., Drysdale, R.A., Harris, N.L., Richter, J., Russo, S., Schroeder, A.J., Shu, S.Q., Stapleton, M., Yamada, C., Ashburner, M., Gelbart, W.M., Rubin, G.M. and Lewis, S.E.

**TITLE** Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review

**JOURNAL** Genome Biol. 3 (12), RESEARCH0083 (2002)

**PUBMED** [12537572](#)

**REMARK** GENOME REANNOTATION.

**REFERENCE** 5 (residues 1 to 250)

**AUTHORS** Munch-Petersen, B., Piskur, J. and Sondergaard, L.

**TITLE** Four deoxynucleoside kinase activities from *Drosophila melanogaster* are contained within a single monomeric enzyme, a new multifunctional deoxynucleoside kinase

**JOURNAL** J. Biol. Chem. 273 (7), 3926-3931 (1998)

**PUBMED** [9461577](#)

**REMARK** ENZYME ACTIVITY.

COMMENT [FUNCTION] Deoxyribonucleoside kinase that has a broad specificity phosphorylating thymidine, deoxyadenosine, deoxycytidine and deoxyguanosine. Specificity is higher for pyrimidine nucleosides. Several anti-viral and anti-cancer nucleoside analogs are also efficiently phosphorylated.  
 [CATALYTIC ACTIVITY] ATP + 2'-deoxynucleoside = ADP + 2'-deoxynucleoside 5'-phosphate.  
 [BIOPHYSICOCHEMICAL PROPERTIES] Kinetic parameters: KM=0.9 uM for thymidine; KM=1 uM for deoxycytidine; KM=109 uM for deoxyadenosine; KM=654 uM for deoxyguanosine; Vmax=29.4 mmol/min/mg enzyme with thymidine as substrate; Vmax=28.7 mmol/min/mg enzyme with deoxycytidine as substrate; Vmax=35.5 mmol/min/mg enzyme with deoxyadenosine as substrate; Vmax=37.7 mmol/min/mg enzyme with deoxyguanosine as substrate.  
 [SUBUNIT] Monomer.  
 [INTERACTION] Q9VVY4:fa1; NbExp=1; IntAct=EBI-99670, EBI-188912.  
 [SIMILARITY] Belongs to the DCK/DGK family.

FEATURES Location/Qualifiers

|         |                                                                                                                                                                                                                                                                                                                                         |
|---------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| source  | 1..250<br>/organism="Drosophila melanogaster"<br>/db_xref="taxon:7227"                                                                                                                                                                                                                                                                  |
| gene    | 1..250<br>/gene="dnk"<br>/locus_tag="CG5452"                                                                                                                                                                                                                                                                                            |
| Protein | 1..250<br>/gene="dnk"<br>/locus_tag="CG5452"<br>/product="Deoxynucleoside kinase"<br>/EC_number="2.7.1.145"                                                                                                                                                                                                                             |
| Region  | 1..250<br>/gene="dnk"<br>/locus_tag="CG5452"<br>/region_name="Mature chain"<br>/experiment="experimental evidence, no additional details recorded"<br>/note="Deoxynucleoside kinase. /FTId=PRO_0000175097."                                                                                                                             |
| Region  | 15..17<br>/gene="dnk"<br>/locus_tag="CG5452"<br>/region_name="Hydrogen bonded turn"<br>/experiment="experimental evidence, no additional details recorded"                                                                                                                                                                              |
| Region  | 21..26<br>/gene="dnk"<br>/locus_tag="CG5452"<br>/region_name="Beta-strand region"<br>/experiment="experimental evidence, no additional details recorded"                                                                                                                                                                                |
| Region  | 23..214<br>/gene="dnk"<br>/locus_tag="CG5452"<br>/region_name="TMPK"<br>/note="Thymidine monophosphate kinase (TMPK), also known as thymidylate kinase, catalyzes the phosphorylation of thymidine monophosphate (TMP) to thymidine diphosphate (TDP) utilizing ATP as its preferred phosphoryl donor; cd01672"<br>/db_xref="CDD:30190" |
| Region  | 23..214<br>/gene="dnk"<br>/locus_tag="CG5452"<br>/region_name="dNK"<br>/note="Deoxyribonucleoside kinase (dNK) catalyzes the                                                                                                                                                                                                            |

phosphorylation of deoxyribonucleosides to yield corresponding monophosphates (dNMPs). This family consists of various deoxynucleoside kinases including deoxyribo-cytidine (EC 2.7.1.74), guanosine (EC 2.7.1; cd01673")  
/db\_xref="CDD:30191"

Site 27..34  
/gene="dnk"  
/locus\_tag="CG5452"  
/site\_type="np-binding"  
/inference="non-experimental evidence, no additional details recorded"  
/note="ATP (Potential)."

Region 33..37  
/gene="dnk"  
/locus\_tag="CG5452"  
/region\_name="Helical region"  
/experiment="experimental evidence, no additional details recorded"

Region 41..43  
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/locus\_tag="CG5452"  
/region\_name="Helical region"  
/experiment="experimental evidence, no additional details recorded"

Region 44..46  
/gene="dnk"  
/locus\_tag="CG5452"  
/region\_name="Hydrogen bonded turn"  
/experiment="experimental evidence, no additional details recorded"

Region 47..50  
/gene="dnk"  
/locus\_tag="CG5452"  
/region\_name="Beta-strand region"  
/experiment="experimental evidence, no additional details recorded"

Region 54..57  
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/region\_name="Helical region"  
/experiment="experimental evidence, no additional details recorded"

Region 65..71  
/gene="dnk"  
/locus\_tag="CG5452"  
/region\_name="Helical region"  
/experiment="experimental evidence, no additional details recorded"

Region 73..92  
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/locus\_tag="CG5452"  
/region\_name="Helical region"  
/experiment="experimental evidence, no additional details recorded"

Region 98..105  
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/experiment="experimental evidence, no additional details recorded"

Region 107..112  
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/locus\_tag="CG5452"

Region /region\_name="Helical region"  
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Region 148..154  
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recorded"

## ORIGIN

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121 ngsleggmyn tleewykfie esihvqadli iylrtspeva yerirqrars eescvplkyl
181 qelhelhedw lihqrrpqsc kvlvldadln lenigteyqr sessifdais snqqpspvlv
241 spskrqrvar
```

//

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Apr 17 2007 11:10:07